THE INHERITANCE OF HUSK LENGTH, EAR LENGTH, AND DAYS-TO-SILKING IN MAIZE

BY

WAYNE HENRY FREEMAN

B. S., Kansas State College, 1938
M. S., University of Illinois, 1940

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SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF DOCTOR OF PHILOSPOHY IN AGRONOMY IN THE GRADUATE SCHOOL OF THE UNIVERSITY OF ILLINOIS, 1945

URBANA, ILLINOIS
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I. Introduction

This investigation was outlined to study certain quantitative characters in corn by the use of reciprocal translocations. Many characters of economic importance, such as yield of grain, size of plant, maturity, and resistance to diseases and insects, are quantitative, their expression being the result of multiple factors. Any contribution to the inheritance of these characters is valuable from a practical standpoint and also adds to our knowledge of the nature of quantitative character inheritance.

The use of chromosomal abberations in inheritance studies of quantitative characters is relatively new. Previous studies have been published by Rhoades, using deficiencies and trisomics; Sprague, using inversions; and Burnham and Cartledge, Heyne and Brunson, and Saboe and Hayes, using reciprocal translocations. Inversions and translocations inhibit crossing over so that a greater portion of the chromosome is linked with the break locus. On this account, they are more efficient than qualitative genes in linkage studies. The use of translocations has been enhanced by the development of stocks by Anderson in which the translocation loci are linked with recessive endosperm genes.

Husk length is a character of economic importance in portions of the southern United States where considerable damage to the grain by insects may be encountered if the ears are not well protected by long, tight-fitting husks. Insects of primary importance are the rice weevil, *Sitophilus oryzae*, L., and the corn earworm, *Heliothis armigera*, Hbn. Ear length is a character of economic importance as it is related to yield. Days-to-silking, as a measure of maturity, is important as a factor of adaptation.

II. Experimental Procedure

Two inbred lines of dent corn, Florida 1 and Florida 2, were chosen for this study. In 1944, these lines had husks 27.8 and 26.2 cm. long; ears, 12.6 and 11.9 cm. long; and 72 and 76 days to silking, respectively. Three series of translocations were crossed with each line; namely, (1) *wx* linked with translocation loci in chromosome 9, (2) *pr* linked with translocation loci in chromosome 5, and (3) *su* linked with translocation loci in chromosome 4. The F_1 crosses were grown at the Georgia Coastal Plain Experiment Station, Tifton, Georgia, in 1943, and were backcrossed to stocks which were recessive for the appropriate endosperm gene, and which were short husked, of medium to short ear length, and early.

The backcrosses in the *su* series, for example. were $(+\ L\ Su \times T\ l\ su) \times +\ l\ su$. Testing plants from the contrasted seed classes, *Su* vs. *su*, then becomes a test of linkage of long husk (*L*) genes with chromosome 4 and the chromosome with which it is translocated. Separation of the seed types serves to separate the plants carrying the translocation from the plants carrying the normal chromosome complement, except for crossing over between the translocation locus and the *su* gene. Classification of normal and semisterile plants on the basis of partial pollen sterility is therefore unnecessary.

The contrasted seed types of the backcrosses were planted in paired rows in 1944. Crossovers could be detected by the presence of plants with semisterile ears in the rows with plants bearing normal ears and vice versa. The numbers of crossovers found were small. Each backcross progeny involving one line and one translocation was considered a separate experiment, the paired rows being planted separately from the progenies of other backcrosses.

The data were treated statistically by analysis of variance and the significance of the differences between the normal and the semisterile populations was determined by

the F test. When populations including more than one backcross parent were analyzed, unadjusted means of the classes were used, as populations of normal and semisterile plants were quite often disproportionate.

Twenty different translocations were crossed with Florida 1 and 19 with Florida 2. Twenty-five different translocations were used in the 39 crosses. The number of plants in the backcross populations ranged from 68 to 422, a total of 12,191 plants being measured.

III. Results and Conclusions

Table 1 presents a summary of the significance of the differences obtained by the application of the F test.

Differences in husk length between the normal and semisterile plants were statistically significant in progenies of 9 of the 20 crosses with Florida 1 and in 10 of the 19 crosses with Florida 2. Genes for long husks in Florida 1 appear to be located in chromosome 1, in chromosome 2, and in chromosome 8; and in Florida 2, in chromosome 1, in chromosome 2, and in chromosome 3. This would indicate that at least four different genes or gene groups were responsible for husk length in these portions of the chromosomes of the two lines involved in this study. Gene groups in chromosomes 1 and 2 were common to both inbred lines.

In ten backcross progenies, the mean husk lengths of the semisterile plants were larger than those of the normal plants. Six of these mean differences were in the *su* series and four of these were significant at odds of 99:1. Several possible explanations for these occurrences are: (1) In the translocation stocks of the *su* series, chromosome 4 carried genes for long husk, (2) genes inhibiting husk length are located in chromosome 4 of Florida 1 and 2, (3) complementary action of factors in the tester and translocation stocks, (4) effect of the translocations, or (5) the influence of the *su* gene on husk length. The other four cases in the other series were only significant at the .05

Table 1. Summary of the significance of F values for differences between normal and semisterile plants in backcross progenies.

	Husk Length		Ear Length		Days-to-Silking	
Translocation	Florida 1	Florida 2	Florida 1	Florida 2	Florida 1	Florida 2
wx series						
1-9a	*[1]	0	**	**	0	**
1-9c	*	**	**	**	0	*
2-9b	**	**	0	**	0	**
3-9a	--	**	--	**	--	0
3-9b	--	0	--	0	--	0
3-9c	0	**	**	**	**	**
4-9b	--	0	--	**	--	0
6-9a	0	0	*[1]	**	0	0
6-9 (a-66)	--	*[1]	--	**	--	0
8-9a	*	0	**	**	**	**
9-10b	0	--	0	--	0	--
su series						
1-4a	**[1]	0	**	**	0	0
2-4a	0	--	**	--	0	--
2-4c	0	0	**	**	0	0
4-5b	--	*[1]	--	0	--	0
4-5d	0	--	**	--	0	--
4-6a	**[1]	--	**	--	0	--
4-8a	0	**[1]	**	**	0	0
4-9a	*[1]	**[1]	**	**	*[1]	0
pr series						
1-5a	**	--	**	--	0	--
1-5c	*[1]	0	0	**	0	**
2-5b	0	0	**	**	**	**
3-5b	0	**	**	**	**	**
4-5c	0	*[1]	**	**	**	**
4-5d	0	--	*	--	**	--

0 No significant differences.
* Significant at .05 probability level.
** Significant at .01 probability level.
[1] Means of the semisterile type greater than the normal.

level of probability and, therefore, may have been chance differences, although certain of the above explanations might also apply.

Ear length genes appeared to be carried by chromosomes 4 and 5 in both inbred lines. In Florida 1, additional genes were indicated in chromosome 1, in chromosome 3, and in chromosome 8. Florida 2 had additional genes for long ears in chromosome 9. Other genes may exist in the other chromosomes represented in the translocations with chromosome 9, but they could not be detected because they were masked by the linkage of ear length genes with the translocation loci in chromosome 9.

Data on days-to-silking showed that the Florida lines were 18 to 27 days later than the stocks used as backcross testers. The translocation stocks were not available for comparison, but they were probably at least as early as the stocks used as backcross testers. Genes for days-to-silking in Florida 1 were located in chromosome 3, in chromosome 5, and in chromosome 8. In Florida 2, the same genes were found, and, in addition, genes in chromosomes 1 and 2.

If it can be assumed that genes for any one of the characters studied are of approximately equal value and that the genes for these characters are randomly distributed throughout the chromosome complement so that the tests sampled the two lines in a random manner, the fact that Florida 1 had longer husks and longer ears than Florida 2 may be explained by the presence of more genes for these characters in Florida 1. Similarly, the increase in days-to-silking in Florida 2 over Florida 1 is the result of more genes for late silking.

VITA

The writer was born on a farm near Kirwin, Smith County, Kansas, November 21, 1915. He attended the public schools at Kirwin, Kansas, and was graduated from Kirwin High School in 1933. After farming with his father for one year, he matriculated at Kansas State College in September, 1934, where the degree of Bachelor of Science in Agriculture, with a major in Agronomy, was conferred in May, 1938.

In June, 1938, a position as half-time research assistant in plant breeding was accepted at the University of Illinois. The writer enrolled in the Graduate School of the University of Illinois, receiving the Master of Science degree in February, 1940. He continued his residence work at the University of Illinois until April, 1941, when he accepted a position as Assistant Agronomist in charge of corn breeding at the Mississippi Agricultural Experiment Station. Since that time he has been Associate Agronomist, Mississippi Agricultural Experiment Station, Associate Agronomist, and Agronomist, Division of Cereal Crops and Diseases, Bureau of Plant Industry, Soils and Agricultural Engineering, U. S. Department of Agriculture, being stationed, since February, 1943, at the Georgia Coastal Plain Experiment Station, Tifton, Georgia, in charge of corn breeding.

Fraternal affiliations include Alpha Kappa Lambda, social fraternity, Phi Kappa Phi, Alpha Zeta, Gamma Sigma Delta, and Sigma Xi.

PUBLICATIONS

Freeman, W. H. et al, 1943. Tests of Corn Hybrids and Varieties at Seven Locations in Mississippi, 1942. Miss. Agr. Expt. Sta. Bul. 373.